



#10

SUBSTITUTE SEQUENCE LISTING

<110> PURDUE RESEARCH FOUNDATION

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<120> PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR PRODUCTION

<130> 290.00490101

<140> 09/762,224

<141> 2001-02-02

<150> US 60/095,242

<151> 1998-08-04

<150> US 60/112,405

<151> 1998-12-15

<150> PCT/US99/17702

<151> 1999-08-04

<160> 8

<170> PatentIn version 3.0

<210> 1

<211> 2958

<212> DNA

<213> Ross River virus

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<210> 2

<211> 985

<212> PRT

<213> Ross River virus

<400> 2

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Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr
 35 40 45

Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg
 50 55 60
 Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr
 65 70 75 80
 Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro
 85 90 95
 Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys
 100 105 110
 Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala
 115 120 125
 His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys
 130 135 140
 Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly
 145 150 155 160
 Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu
 165 170 175
 Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val
 180 185 190
 Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val
 195 200 205
 Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr
 210 215 220
 Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile
 225 230 235 240
 Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr
 245 250 255
 Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn
 260 265 270
 Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp
 275 280 285
 Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser
 290 295 300
 Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His
 305 310 315 320
 Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg
 325 330 335
 Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His
 340 345 350
 Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro
 355 360 365
 His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro
 370 375 380

Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val
385 390 395 400

Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro
405 410 415

His Glu Ile Ile Gln Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile
420 425 430

Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala
435 440 445

Thr Cys Cys Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr
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Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys
465 470 475 480

Cys Ala Pro Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr
485 490 495

Leu Trp Asp Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro
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Ala Ala Ala Leu Ala Leu Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys
515 520 525

Cys Cys Lys Pro Phe Ser Phe Leu Val Leu Leu Ser Leu Gly Ala Ser
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Ala Lys Ala Tyr Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe
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Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu
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Gln Leu Glu Val Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu
580 585 590

Tyr Ile Thr Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys
595 600 605

Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln
610 615 620

Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr
625 630 635 640

Cys Phe Cys Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp
645 650 655

Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His
660 665 670

Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn
675 680 685

Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly
690 695 700

Gly Ser Lys Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe
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Asp Asn Lys Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe

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Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu		
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770	775	780
Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr		
785	790	795
Lys Ala Pro Phe Gly Cys Lys Ile Lys Thr Asn Pro Val Arg Ala Met		
805	810	815
Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser		
820	825	830
Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys		
835	840	845
Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr		
850	855	860
Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His		
865	870	875
Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp		
885	890	895
Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe		
900	905	910
Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu		
915	920	925
Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln		
930	935	940
Val Phe Pro Asp Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu		
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Ala Ser Gly Leu Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val		
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Leu Val Thr Cys Ile Thr Met Arg Arg		
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<210> 3

<211> 2224

<212> DNA

<213> Ebola virus

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	120

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<210> 4

<211> 676

<212> PRT

<213> Ebola virus

<400> 4

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Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr
130 135 140

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
245 250 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

Glu Leu Ser Phe Thr Val Val Ser Asn Gly Ala Lys Asn Ile Ser Gly
305 310 315 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
325 330 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
340 345 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
355 360 365

Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly Pro
370 375 380

Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu
385 390 395 400

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser Thr
405 410 415

Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro Pro Lys Ala
420 425 430

Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala Thr
435 440 445

Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
450 455 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465 470 475 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
485 490 495

Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
500 505 510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
515 520 525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
530 535 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545 550 555 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr

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Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys		
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Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp		
610	615	620
Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp		
625	630	635
Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile		
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Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys		
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Lys Phe Val Phe		
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<210> 5
<211> 2103
<212> DNA
<213> Marburg virus

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ccc	2103

<210> 6

<211> 681

<212> PRT

<213> Marburg virus

<400> 6

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
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 20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
 35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
195 200 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
210 215 220

Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
225 230 235 240

Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr
245 250 255

Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
260 265 270

Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
275 280 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
290 295 300

Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
305 310 315 320

Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
325 330 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
340 345 350

Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
355 360 365

Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
370 375 380

Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys

385	390	395	400
Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser			
405		410	415
Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg			
420		425	430
Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu			
435	440	445	
Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr			
450	455	460	
Lys Thr Ile Phe Asp Glu Ser Ser Ser Gly Ala Ser Ala Glu Glu			
465	470	475	480
Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro			
485		490	495
Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys			
500		505	510
Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala			
515		520	525
Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr			
530	535	540	
Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg			
545	550	555	560
Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val			
565		570	575
Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp			
580		585	590
Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp			
595		600	605
Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile			
610		615	620
Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu			
625	630	635	640
Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly			
645		650	655
Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile			
660		665	670
Cys Arg Ile Phe Thr Lys Tyr Ile Gly			
675		680	

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<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 7

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25

<210> 8

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<213> Artificial

<220>

<223> Primer

<400> 8

cgctctagat taccgacgca ttgttatg

28